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RAW SEQUENCE LISTING   DATE: 05/01/2002
PATENT APPLICATION: US/10/090,378   TIME: 11:53:16

Input Set : N:\Crf3\RULE60\10090378.raw
Output Set: N:\CRF3\05012002\J090378.raw

```
 1 <110> APPLICANT: Panganiban, Antonito
 2       Callahan, Mark A.
 3 <120> TITLE OF INVENTION: Method of Identifying Modulators of HIV-1 VPU and GAG
 4       Interaction with U Binding Protein (UBP)
 5 <130> FILE REFERENCE: 960296:95335
 6 <140> CURRENT APPLICATION NUMBER: 10/090,378
 7 <141> CURRENT FILING DATE: 2002-03-04
 9 <150> PRIOR APPLICATION NUMBER: US/09/301,978C
10 <151> PRIOR FILING DATE: 1999-04-29
13 <150> PRIOR APPLICATION NUMBER: 60/083,567
14 <151> PRIOR FILING DATE: 1998-04-30
15 <160> NUMBER OF SEQ ID NOS: 29
16 <170> SOFTWARE: PatentIn Ver. 2.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 2221
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
22 <220> FEATURE:
23 <221> NAME/KEY: unsure
24 <222> LOCATION: (1514)
25 <223> OTHER INFORMATION: n = any nucleotide.
26 <221> NAME/KEY: unsure
27 <222> LOCATION: (2066)
28 <223> OTHER INFORMATION: n = any nucleotide.
29 <400> 1
30       tcggtcgcct gagaggtatc acctcttctg ggctcaagat ggacaacaag aagcgcctgg 60
31       cctacgccat catccagttc ctgcatgacc agctccggca cggggcctc tcgtccgatg 120
32       ctcaggagag cttggaagtc gccatccagt gcctggagac tgcgtttggg gtgacggtag 180
33       aagacagtga ccttgcgctc cctcagactc tgccggagat atttgaagcg gctgccacgg 240
34       gcaaggagat gccgcaggac ctgaggagcc cagcgcgaac cccgccttcc gaggaggact 300
35       cagcagaggc agagcgcctc aaaaccgaag gaaacgagca gatgaaagtg gaaaactttg 360
36       aagctgccgt gcatttctac ggaaaagcca tcgagctcaa cccagccaac gccgtctatt 420
37       tctgcaacag agccgcagcc tacagcaaac tcggcaacta cgcaggcgcg gtgcaggact 480
38       gtgagcgggc catctgcatt gacccggcct acagcaaggc ctacggcagg atgggcctgg 540
39       cgctctccag cctcaacaag cacgtggagg ccgtggctta ctacaagaag gcgctggagc 600
40       tggaccccga caacgagaca tacaagtcca acctcaagat agcggagctg aagctgcggg 660
41       aggcccccag ccccacggga ggcgtgggca gcttcgacat cgccggcctg ctgaacaacc 720
42       ctggcttcat gagcatggct tcgaacctaa tgaacaatcc ccagattcag cagctcatgt 780
43       ccggcatgat ttcgggtggc aacaaccct tgggaactcc cggcaccagc ccctcgcaga 840
44       acgacctggc cagcctcatc caggcgggcc agcagtttgc ccagcagatg cagcagcaga 900
45       acccagagtt gatagagcag ctcaggagcc aatccggagt cggacgccca gcgccagcaa 960
46       cgacgaccag caggagtgac gctgcctgct cccggtgtga ccgcgtcctt ccctggccga 1020
47       cccgaaggaa gccttctggt tgtctgccac ttcctcctgt tggactgcct gagagagggg 1080
```

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```
       48        aagagagaga cctcggacct gcatgtcaag atggattttc cccttttatc tctgccctcc 1140
       49        tccactccct ttttgtaact cccttacagc ccccagaccc ttcttgaaac gagagccagc 1200
       50        aagctgagca cagaccagca gcgacctccc ttccagcccc cagaaagctc ggtcacttga 1260
       51        gtgttttcta gaatcctggg gtgctcccgg gccgctctca gagaagtggc aggtttcacg 1320
       52        ttcagccgtg tggcggatcg tgtggcttcc aaagcctttt acagcccccg cccccatcc 1380
       53        cgtggtctgt ctgcaggaac tctcccgtct gtgagaagcc tctttccgag tcgacctccc 1440
       54        ggccaccccg ccctgtgcc tgctcggaag agctcactgc cagctgcggc ctgggcaccg 1500
W--> 55        cgggccatgt gtgnttgcat gaggaactct ttagtggcag acacctaaga gacggctgcg 1560
       56        gtcaccccac gcctccgtgg ctcaggagcc gtcctgggtg cataggacca gtttctgtga 1620
       57        cttttctcca gttgggcatg ttgacagaca tgtttcccct cctcccaccc tcattttctg 1680
       58        gtcctcgcga ctgagagcca ggggcgacat catgaccttc tgtcccggcc gccttagccc 1740
       59        cgggaacagg gaagggagct gggccgtttc tgtctgtgtc ccatcctgct gtccttctgt 1800
       60        cctggatgtt tcatgggccc ggggcccccc agggaagctt acccctcctg tgctgggtgg 1860
       61        aggccacggg acacctcagg tgccacccac cttggcccta aaacagccac caggaaagca 1920
       62        gccggagagc cggacagcgg gcagcctgtc tgggttcctg aggcctgggg gtggcagacg 1980
       63        aacccacggc gccgtggtcc cagcagcagg gttgtcagtc ggagcatcct ggggctccct 2040
W--> 64        ggctcctggc cgtctgtgag gtaggngcag taccgtgtat cgtaggtagc agtaggaacg 2100
       65        ggggccaccg cggccctgca gccgttcatg gcggtgaggt gtgtgccaag cccacccggg 2160
       66        gtgcagggcg tgacgtgtgg ggaataaata ggcgttgtga cctcaaaaaa aaaaaaaaaa 2220
       67        a                                                                  2221
```

69 <210> SEQ ID NO: 2
70 <211> LENGTH: 382
71 <212> TYPE: PRT
72 <213> ORGANISM: Homo sapiens
73 <400> SEQUENCE: 2

```
74        Met Asp Asn Lys Lys Arg Leu Ala Tyr Ala Ile Ile Gln Phe Leu His
75          1               5                   10                  15
76        Asp Gln Leu Arg His Gly Gly Leu Ser Ser Asp Ala Gln Glu Ser Leu
77                        20                  25                  30
78        Glu Val Ala Ile Gln Cys Leu Glu Thr Ala Phe Gly Val Thr Val Glu
79                    35                  40                  45
80        Asp Ser Asp Leu Ala Leu Pro Gln Thr Leu Pro Glu Ile Phe Glu Ala
81                50                  55                  60
82        Ala Ala Thr Gly Lys Glu Met Pro Gln Asp Leu Arg Ser Pro Ala Arg
83            65                  70                  75                  80
84        Thr Pro Pro Ser Glu Glu Asp Ser Ala Glu Ala Glu Arg Leu Lys Thr
85                        85                  90                  95
86        Glu Gly Asn Glu Gln Met Lys Val Glu Asn Phe Glu Ala Ala Val His
87                        100                 105                 110
88        Phe Tyr Gly Lys Ala Ile Glu Leu Asn Pro Ala Asn Ala Val Tyr Phe
89                115                 120                 125
90        Cys Asn Arg Ala Ala Ala Tyr Ser Lys Leu Gly Asn Tyr Ala Gly Ala
91            130                 135                 140
92        Val Gln Asp Cys Glu Arg Ala Ile Cys Ile Asp Pro Ala Tyr Ser Lys
93          145                 150                 155                 160
94        Ala Tyr Gly Arg Met Gly Leu Ala Leu Ser Ser Leu Asn Lys His Val
95                        165                 170                 175
96        Glu Ala Val Ala Tyr Tyr Lys Lys Ala Leu Glu Leu Asp Pro Asp Asn
97                    180                 185                 190
```

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Input Set : N:\Crf3\RULE60\10090378.raw
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```
98        Glu Thr Tyr Lys Ser Asn Leu Lys Ile Ala Glu Leu Lys Leu Arg Glu
99                195                 200                 205
100       Ala Pro Ser Pro Thr Gly Gly Val Gly Ser Phe Asp Ile Ala Gly Leu
101           210                 215                 220
102       Leu Asn Asn Pro Gly Phe Met Ser Met Ala Ser Asn Leu Met Asn Asn
103       225                 230                 235                 240
104       Pro Gln Ile Gln Gln Leu Met Ser Gly Met Ile Ser Gly Gly Asn Asn
105                           245                 250                 255
106       Pro Leu Gly Thr Pro Gly Thr Ser Pro Ser Gln Asn Asp Leu Ala Ser
107                   260                 265                 270
108       Leu Ile Gln Ala Gly Gln Gln Phe Ala Gln Gln Met Gln Gln Gln Asn
109                   275                 280                 285
110       Pro Glu Leu Ile Glu Gln Leu Arg Ser Gln Ser Gly Val Gly Arg Pro
111           290                 295                 300
112       Ala Pro Ala Thr Thr Thr Ser Arg Ser Asp Ala Ala Cys Ser Arg Cys
113       305                 310                 315                 320
114       Asp Arg Val Leu Pro Trp Pro Thr Arg Arg Lys Pro Ser Gly Cys Leu
115                   325                 330                 335
116       Pro Leu Pro Pro Val Gly Leu Pro Glu Arg Gly Glu Glu Arg Asp Leu
117                   340                 345                 350
118       Gly Pro Ala Cys Gln Asp Gly Phe Ser Pro Phe Ile Ser Ala Leu Leu
119                   355                 360                 365
120       His Ser Leu Phe Val Thr Pro Leu Gln Pro Pro Asp Pro Ser
121           370                 375                 380
123 <210> SEQ ID NO: 3
124 <211> LENGTH: 23
125 <212> TYPE: DNA
126 <213> ORGANISM: Artificial Sequence
127 <220> FEATURE:
128 <223> OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide
129       Primer
130 <400> SEQUENCE: 3
131       agtagtacat catatgcaac cta                                    23
133 <210> SEQ ID NO: 4
134 <211> LENGTH: 21
135 <212> TYPE: DNA
136 <213> ORGANISM: Artificial Sequence
137 <220> FEATURE:
138 <223> OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide
139       Primer
140 <400> SEQUENCE: 4
141       tccacacagg atccccataa t                                      21
143 <210> SEQ ID NO: 5
144 <211> LENGTH: 31
145 <212> TYPE: DNA
146 <213> ORGANISM: Artificial Sequence
147 <220> FEATURE:
148 <223> OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide
149       Primer
```

RAW SEQUENCE LISTING   DATE: 05/01/2002
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            Input Set : N:\Crf3\RULE60\10090378.raw
            Output Set: N:\CRF3\05012002\J090378.raw

```
150 <400> SEQUENCE: 5
151        cgggatccgg tgcgagagcg tcggtattaa g                          31
153 <210> SEQ ID NO: 6
154 <211> LENGTH: 28
155 <212> TYPE: DNA
156 <213> ORGANISM: Artificial Sequence
157 <220> FEATURE:
158 <223> OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide
159        Primer
160 <400> SEQUENCE: 6
161        gctctagacc tgtatctaat agagcttc                              28
163 <210> SEQ ID NO: 7
164 <211> LENGTH: 21
165 <212> TYPE: DNA
166 <213> ORGANISM: Artificial Sequence
167 <220> FEATURE:
168 <223> OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide
169        Primer
170 <400> SEQUENCE: 7
171        ggccagatga gagaaccaag g                                     21
173 <210> SEQ ID NO: 8
174 <211> LENGTH: 27
175 <212> TYPE: DNA
176 <213> ORGANISM: Artificial Sequence
177 <220> FEATURE:
178 <223> OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide
179        Primer
180 <400> SEQUENCE: 8
181        caaagagtga cttaagggaa gctaaag                               27
183 <210> SEQ ID NO: 9
184 <211> LENGTH: 21
185 <212> TYPE: DNA
186 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide
189        Primer
190 <400> SEQUENCE: 9
191        cctatagctt tatgtccgca g                                     21
193 <210> SEQ ID NO: 10
194 <211> LENGTH: 27
195 <212> TYPE: DNA
196 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <223> OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide
199        Primer
200 <400> SEQUENCE: 10
201        ctttagcttc ccttaagtca ctctttg                               27
203 <210> SEQ ID NO: 11
204 <211> LENGTH: 34
```

```
        205 <212> TYPE: PRT
        206 <213> ORGANISM: Artificial Sequence
        207 <220> FEATURE:
        208 <223> OTHER INFORMATION: Description of Artificial Sequence:TPR Motifs
        209       Consensus Sequence
W--> 210 <221> NAME/KEY: UNSURE
        211 <222> LOCATION: (1)
        212 <223> OTHER INFORMATION: Can be any large hydrophobic amino acid.
W--> 213 <221> UNSURE
        214 <222> LOCATION: (2)..(3)
        215 <223> OTHER INFORMATION: Can be any amino acid.
W--> 216 <221> UNSURE
        217 <222> LOCATION: (4)
        218 <223> OTHER INFORMATION: Can be any large hydrophobic amino acid.
W--> 219 <221> VARIANT
        220 <222> LOCATION: (5)
        221 <223> OTHER INFORMATION: Can be an Alanine as well.
W--> 222 <221> UNSURE
        223 <222> LOCATION: (6)
        224 <223> OTHER INFORMATION: Can be any amino acid.
W--> 225 <221> UNSURE
        226 <222> LOCATION: (7)
        227 <223> OTHER INFORMATION: Can be any large hydrophobic amino acid.
W--> 228 <221> VARIANT
        229 <222> LOCATION: (8)
        230 <223> OTHER INFORMATION: Can be a Phenylalanine as well.
W--> 231 <221> UNSURE
        232 <222> LOCATION: (9)..(13)
        233 <223> OTHER INFORMATION: Can be any amino acid.
W--> 234 <221> UNSURE
        235 <222> LOCATION: (14)
        236 <223> OTHER INFORMATION: Can be any large hydrophobic amino acid.
W--> 237 <221> UNSURE
        238 <222> LOCATION: (15)..(16)
        239 <223> OTHER INFORMATION: Can be any amino acid.
W--> 240 <221> UNSURE
        241 <222> LOCATION: (18)
        242 <223> OTHER INFORMATION: Can be any large hydrophobic amino acid.
W--> 243 <221> UNSURE
        244 <222> LOCATION: (19)..(20)
        245 <223> OTHER INFORMATION: Can be any amino acid.
W--> 246 <221> VARIANT
        247 <222> LOCATION: (21)
        248 <223> OTHER INFORMATION: Can be Tyrosine as well.
W--> 249 <221> UNSURE
        250 <222> LOCATION: (22)..(23)
        251 <223> OTHER INFORMATION: Can be any amino acid.
W--> 252 <221> UNSURE
        253 <222> LOCATION: (25)
```

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<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 1514,2066
Seq#:11; Xaa Pos. 1,2,3,4,6,7,9,10,11,12,13,14,15,16,18,19,20,22,23,25,26
Seq#:11; Xaa Pos. 27,28,30,31,32,33,34

```
                    VERIFICATION SUMMARY              DATE: 05/01/2002
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                    Input Set : N:\Crf3\RULE60\10090378.raw
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L:29 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:55 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1500
L:64 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:2040
L:210 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:213 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:216 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:219 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:222 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:225 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:228 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:231 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:234 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:237 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:240 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:243 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:246 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:249 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:252 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:255 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:258 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:261 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:264 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:267 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:16
L:272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:32
```